

[illegible]

(ii) TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods

(iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: DNAX Research Institute
 (B) STREET: 901 California Avenue
 (C) CITY: Palo Alto
 (D) STATE: California
 (E) COUNTRY: USA
 (F) ZIP: 94304-1104

(vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: US
 (B) FILING DATE: 08-MAR-1999
 (C) CLASSIFICATION:

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 852-9196
(B) TELEFAX: (650) 496-1200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 132..1064

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 567
(D) OTHER INFORMATION: /note= "nucleotides 567, 573, 1336, 1342, and 1369 designated C, but each may be A, C, G, or T"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 643
(D) OTHER INFORMATION: /note= "nucleotides 643, 1287, and 1290 designated C, but each may be C or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 772
(D) OTHER INFORMATION: /note= "nucleotides 772, 806, and 1261 designated G, but each may be A or G"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1236
(D) OTHER INFORMATION: /note= "nucleotides 1236, 1260, 1282, and 1289 are designated T, but each may be G or T"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1247
(D) OTHER INFORMATION: /note= "nucleotides 1247, 1257, 1293, and 1302 designated C, but each may be C or T"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1266
(D) OTHER INFORMATION: /note= "nucleotides 1266 and 1298 designated T, but each may be A or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGACCCACG CGTCCGCGCT GCGACTCAGA CCTCAGCTCC AACATATGCA TTCTGAAGAA	60
AGATGGCTGA GATGGACAGA ATGCTTTATT TTGGAAAGAA ACAATGTTCT AGGTCAAAC	120
GAGTCTACCA A ATG CAG ACT TTC ACA ATG GTT CTA GAA GAA ATC TGG ACA	170
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr	
1 5 10	
AGT CTT TTC ATG TGG TTT TTC TAC GCA TTG ATT CCA TGT TTG CTC ACA	218
Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr	
15 20 25	

GAT	GAA	GTG	GCC	ATT	CTG	CCT	GCC	CCT	CAG	AAC	CTC	TCT	GTA	CTC	TCA	266
Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
30					35					40					45	
ACC	AAC	ATG	AAG	CAT	CTC	TTG	ATG	TGG	AGC	CCA	GTG	ATC	GCG	CCT	GGA	314
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly	
				50					55					60		
GAA	ACA	GTG	TAC	TAT	TCT	GTC	GAA	TAC	CAG	GGG	GAG	TAC	GAG	AGC	CTG	362
Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu	
			65					70					75			
TAC	ACG	AGC	CAC	ATC	TGG	ATC	CCC	AGC	AGC	TGG	TGC	TCA	CTC	ACT	GAA	410
Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu	
		80					85					90				
GGT	CCT	GAG	TGT	GAT	GTC	ACT	GAT	GAC	ATC	ACG	GCC	ACT	GTG	CCA	TAC	458
Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr	
	95					100					105					
AAC	CTT	CGT	GTC	AGG	GCC	ACA	TTG	GGC	TCA	CAG	ACC	TCA	GCC	TGG	AGC	506
Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser	
110					115					120					125	
ATC	CTG	AAG	CAT	CCC	TTT	AAT	AGA	AAC	TCA	ACC	ATC	CTT	ACC	CGA	CCT	554
Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro	
				130					135					140		
GGG	ATG	GAG	ATC	CCC	AAA	CAT	GGC	TTC	CAC	CTG	GTT	ATT	GAG	CTG	GAG	602
Gly	Met	Glu	Ile	Pro	Lys	His	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu	
			145					150					155			
GAC	CTG	GGG	CCC	CAG	TTT	GAG	TTC	CTT	GTG	GCC	TAC	TGG	ACG	AGG	GAG	650
Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Thr	Arg	Glu	
	160						165					170				
CCT	GGT	GCC	GAG	GAA	CAT	GTC	AAA	ATG	GTG	AGG	AGT	GGG	GGT	ATT	CCA	698
Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	
	175					180					185					
GTG	CAC	CTA	GAA	ACC	ATG	GAG	CCA	GGG	GCT	GCA	TAC	TGT	GTG	AAG	GCC	746
Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	
190					195				200						205	
CAG	ACA	TTC	GTG	AAG	GCC	ATT	GGG	AGG	TAC	AGC	GCC	TTC	AGC	CAG	ACA	794
Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	
				210				215						220		
GAA	TGT	GTG	GAG	GTG	CAA	GGA	GAG	GCC	ATT	CCC	CTG	GTA	CTG	GCC	CTG	842
Glu	Cys	Val	Glu	Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	
			225					230					235			
TTT	GCC	TTT	GTT	GGC	TTC	ATG	CTG	ATC	CTT	GTG	GTC	GTG	CCA	CTG	TTC	890
Phe	Ala	Phe	Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	

66000" 01553260

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..694

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 193

(D) OTHER INFORMATION: /note= "nucleotide 193 designated
C, may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

C	CGG	GTC	GAC	CCA	CGC	GTC	CGC	CTG	GTT	TCC	CCC	TGG	CTG	ACA	GTG	46
	Arg	Val	Asp	Pro	Arg	Val	Arg	Leu	Val	Ser	Pro	Trp	Leu	Thr	Val	
	1				5					10					15	
CCT	TGG	TTC	CTG	TCC	TGT	TGG	AAT	GTT	ACC	ATT	GGG	CCT	CCT	GAG	AGC	94
Pro	Trp	Phe	Leu	Ser	Cys	Trp	Asn	Val	Thr	Ile	Gly	Pro	Pro	Glu	Ser	
			20						25					30		
ATC	TGG	GTG	ACG	CCG	GGA	GAA	GCC	TCC	CTC	ATC	ATC	AGG	TTC	TCC	TCT	142
Ile	Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	
			35					40					45			
CCC	TTC	GAC	GTC	CCT	CCC	AAC	CTG	GGC	TAT	TTC	CAG	TAC	TAT	GTC	CAT	190
Pro	Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	
		50					55					60				
TAC	TGG	GAA	AAG	GCG	GGA	ATC	CAA	AAG	GTT	AAA	GGT	CCT	TTC	AAG	AGC	238
Tyr	Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	
	65					70					75					
AAC	TCC	ATC	GTG	TTG	GAT	GGC	TTG	AGA	CCC	TTA	AGA	GAA	TAC	TGT	TTA	286
Asn	Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	
	80				85				90					95		
CAA	GTG	AAG	GCG	CAT	CTC	TTT	CGC	ACA	TCC	TGC	AAC	ACC	TCT	AGG	CCC	334
Gln	Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	
			100						105					110		
GGC	CGC	TTA	AGC	AAC	ATA	ACT	TGC	TAC	GAA	ACA	ATG	ATG	GAT	GCC	ACT	382
Gly	Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	
			115					120					125			
ACG	AAG	CTT	CAA	CAA	GTC	ATC	CTC	ATC	GCC	GTG	GGA	GTC	TTT	CTG	TCG	430
Thr	Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	
		130					135					140				
CTG	GCG	GCG	CTG	GCG	GGG	GGC	TGT	TTC	TTC	CTG	GTG	CTG	AGA	TAC	AAA	478
Leu	Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	

155

GGC CTG GTG AAA TAC TGG TTT CAC TCT CCG CCA AGC ATC CCA TCA CAA 526
 Gly Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln
 160 165 170 175

ATC GAA GAG TAT CTG AAG GAC CCG AGC CAG CCT ATC CTA GAG GCC CTG 574
Ile Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu
180 185 190

GAC AAG GAC ACG TCA CCA ACA GAT GAT GCC TGG GAC TTG GTG TCT GTT 622
Asp Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val
195 200 205

GTT GCA TTT CCA GCA AAG GAG CAA GAA GAT GTT CCC CAA AGC ACT TTG 670
Val Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu
210 215 220

ACC CAA AAC TCT GGT GCG GTC TGC TAGCCTGTGG GGTAAGGGCT CTGAGCCGAG 724
Thr Gln Asn Ser Gly Ala Val Cys
225 230

GAAGCTGCTG ATGTCCATGT CAGCACTTTA TGGAAATCCGG TCCTCCATTT TCCTGTCCCC 784

AAAAGGCCCG TCAGTGCCTG TGAAGATGTA ACGGGTCTCA TGGGGGCGAC AAGCTTATTG 844

ATTTTTTCT TCAAATAAG AGTTTTCTAA TCATACGCGT TTTTAGAATA ATTCTACAGA 904

TATGTCCCCG AAAGATTAAG ATTTCTCTTA AACACTAAAA AGACATGTAA TTATTTGTTA 964

GCAAATGGGC GTCTGGCACG CCTCTGACAC TTTTTCGTCA GCAGCCAGGA CACGAGGTCC 1024

CCTCCTTGAT GAAGCCCCTC GGGCAGACCA TGTCACCTGT CCCAGCCTGC CCCAAGAAGG 1084

GACATTAAGT GGCCCTTCTT CATATCCAAA CACCTGGCTT GAAATGTGAT TAGCCCTGTA 1144

AATAGTTTCA CAGAGATTAA GCCTTTTTTTT CCCCCAAGTT AGGAATAAAA GACTATAATT 1204

AACTTTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1244

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
1 5 10 15

Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 20 25 30
 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 35 40 45
 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr
 50 55 60
 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 65 70 75 80
 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
 85 90 95
 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
 100 105 110
 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
 115 120 125
 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
 130 135 140
 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
 145 150 155 160
 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
 165 170 175
 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
 180 185 190
 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
 195 200 205
 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
 210 215 220
 Gln Asn Ser Gly Ala Val Cys
 225 230

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00000155000

0 **1** **2** **3** **4** **5** **6** **7** **8** **9**

Met	Arg	Pro	Thr	Leu	Leu	Trp	Ser	Leu	Leu	Leu	Gly	Val	Phe	1	5	10	15	
Ala	Ala	Ala	Ala	Ala	Ala	Pro	Pro	Asp	Pro	Leu	Ser	Gln	Leu	Pro	Ala	20	25	30
Pro	Gln	His	Pro	Lys	Ile	Arg	Leu	Tyr	Asn	Ala	Glu	Gln	Val	Leu	Ser	35	40	45
Trp	Glu	Pro	Val	Ala	Leu	Ser	Asn	Ser	Thr	Arg	Pro	Val	Val	Tyr	Arg	50	55	60
Val	Gln	Phe	Lys	Tyr	Thr	Asp	Ser	Lys	Trp	Phe	Thr	Ala	Asp	Ile	Met	65	70	75
Ser	Ile	Gly	Val	Asn	Cys	Thr	Gln	Ile	Thr	Ala	Thr	Glu	Cys	Asp	Phe	85	90	95
Thr	Ala	Ala	Ser	Pro	Ser	Ala	Gly	Phe	Pro	Met	Asp	Phe	Asn	Val	Thr	100	105	110
Leu	Arg	Leu	Arg	Ala	Glu	Leu	Gly	Ala	Leu	His	Ser	Ala	Trp	Val	Thr	115	120	125
Met	Pro	Trp	Phe	Gln	His	Tyr	Arg	Asn	Val	Thr	Val	Gly	Pro	Pro	Glu	130	135	140
Asn	Ile	Glu	Val	Thr	Pro	Gly	Glu	Gly	Ser	Leu	Ile	Ile	Arg	Phe	Ser	145	150	155
Ser	Pro	Phe	Asp	Ile	Ala	Asp	Thr	Ser	Thr	Ala	Phe	Phe	Cys	Tyr	Tyr	165	170	175
Val	His	Tyr	Trp	Glu	Lys	Gly	Gly	Ile	Gln	Gln	Val	Lys	Gly	Pro	Phe	180	185	190
Arg	Ser	Asn	Ser	Ile	Ser	Leu	Asp	Asn	Leu	Lys	Pro	Ser	Arg	Val	Tyr	195	200	205
Cys	Leu	Gln	Val	Gln	Ala	Gln	Leu	Leu	Trp	Asn	Lys	Ser	Asn	Ile	Phe	210	215	220
Arg	Val	Gly	His	Leu	Ser	Asn	Ile	Ser	Cys	Tyr	Glu	Thr	Met	Ala	Asp	225	230	235
Ala	Ser	Thr	Glu	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ser	Val	Gly	Thr	Phe	245	250	255
Ser	Leu	Leu	Ser	Val	Leu	Ala	Gly	Ala	Cys	Phe	Phe	Leu	Val	Leu	Lys	260	265	270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
275 280 285

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
305 310 315 320

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
325 330 335

Leu

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
115 120 125

[illegible]

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala
 210 215 220
 Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
 225 230 235 240
 Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe
 245 250 255
 Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His
 260 265 270
 Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu
 275 280 285
 Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser
 290 295 300
 Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly
 305 310 315 320
 Gln Gly Pro Gln Ser
 325

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